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NEWS 2 NOV 21 CAS patent coverage to include exemplified prophetic
substances identified in English-, French-, German-,
and Japanese-language basic patents from 2004-present
NEWS 3 NOV 26 MARPAT enhanced with FSORT command
NEWS 4 NOV 26 CHEMSAFE now available on STN Easy
NEWS 5 NOV 26 Two new SET commands increase convenience of STN
searching
NEWS 6 DEC 01 ChemPort single article sales feature unavailable
NEWS 7 DEC 12 GBFULL now offers single source for full-text
coverage of complete UK patent families
NEWS 8 DEC 17 Fifty-one pharmaceutical ingredients added to FS
NEWS 9 JAN 06 The retention policy for unread STNmail messages
will change in 2009 for STN-Columbus and STN-Tokyo
NEWS 10 JAN 07 WPIIDS, WPINDEXT, and WPIX enhanced Japanese Patent
Classification Data
NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,
AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.
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NEWS IPC8 For general information regarding STN implementation of IPC 8

Enter NEWS followed by the item number or name to see news on that
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***** STN Columbus *****

FILE 'HOME' ENTERED AT 23:44:57 ON 01 FEB 2009

=> index bioscience medicine

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
0.22	0.22

FULL ESTIMATED COST

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIORNG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CAB, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDPB, DDFU, DGENE, DISSABS, DRUGB,

71 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view
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=> s t7 (3a)(endo or endonucleas?) (3a) (1 or i)

2 FILE AGRICOLA
5 FILE BIOENG
62 FILE BIOSIS
18 FILE BIOTECHABS
18 FILE BIOTECHDS
27 FILE BIOTECHNO

13 FILES SEARCHED...

88 FILE CAPLUS
59 FILE DGENE
2 FILE DISSABS
1 FILE DRUGU

27 FILES SEARCHED...

50 FILE EMBASE
38 FILE EMBIOBASE
57 FILE GENBANK

35 FILES SEARCHED...

34 FILE IFIPAT
40 FILE LIFESCI
56 FILE MEDLINE
12 FILE PASCAL

51 FILES SEARCHED...

66 FILE SCISEARCH
21 FILE TOXCENTER
25 FILE USGENE
103 FILE USPATFULL

61 FILES SEARCHED...

14 FILE USPAT2
25 FILE WPIDS
25 FILE WPINDEX

24 FILES HAVE ONE OR MORE ANSWERS, 71 FILES SEARCHED IN STNINDEX

L1 QUE T7 (3A)(ENDO OR ENDONUCLEAS?) (3A) (1 OR I)

=> d rank

F1 103 USPATFULL
F2 88 CAPLUS
F3 66 SCISEARCH
F4 62 BIOSIS
F5 59 DGENE
F6 57 GENBANK
F7 56 MEDLINE
F8 50 EMBASE
F9 40 LIFESCI
F10 38 EMBIOBASE
F11 34 IFIPAT
F12 27 BIOTECHNO
F13 25 USGENE
F14 25 WPIDS
F15 25 WPINDEX
F16 21 TOXCENTER
F17 18 BIOTECHABS
F18 18 BIOTECHDS
F19 14 USPAT2

F20	12	PASCAL
F21	5	BIOENG
F22	2	AGRICOLA
F23	2	DISSABS
F24	1	DRUGU

-> file f1-f4, f7-15

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

FULL ESTIMATED COST

4.08

4.30

FILE 'USPATFULL' ENTERED AT 23:48:56 ON 01 FEB 2009

CA INDEXING COPYRIGHT (C) 2009 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'CAPLUS' ENTERED AT 23:48:56 ON 01 FEB 2009

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FILE 'IFIPAT' ENTERED AT 23:48:56 ON 01 FEB 2009

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FILE 'BIOTECHNO' ENTERED AT 23:48:56 ON 01 FEB 2009

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FILE 'WPIDS' ENTERED AT 23:48:56 ON 01 FEB 2009

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FILE 'WPINDEX' ACCESS NOT AUTHORIZED

-> s t7 (3a)(endo or endonucleas?) (3a) (1 or i)

8 FILES SEARCHED...

L2 614 T7 (3A) (ENDO OR ENDONUCLEAS?) (3A) (1 OR I)

-> s l2(s)(modif? or muta? or delet? or inser?)

11 FILES SEARCHED...

L3 203 L2(S) (MODIF? OR MUTA? OR DELET? OR INSER?)

-> s l3 and beta?

L4 89 L3 AND BETA?

-> dup rem l4
 DUPLICATE IS NOT AVAILABLE IN 'USGENE'.
 ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
 PROCESSING COMPLETED FOR L4
 L5 74 DUP REM L4 (15 DUPLICATES REMOVED)

-> d ti l5 1-74

L5 ANSWER 1 OF 74 USPATFULL on STN
 TI DETECTION OF TARGET MOLECULES THROUGH INTERACTION WITH PROBES

L5 ANSWER 2 OF 74 USPATFULL on STN
 TI Cell Free Biosynthesis of High-Quality Nucleic Acid and Uses Thereof

L5 ANSWER 3 OF 74 USPATFULL on STN
 TI Methods and Compositions for Assessment of Pulmonary Function and Disorders

L5 ANSWER 4 OF 74 USPATFULL on STN
 TI Enrichment Through Heteroduplexed Molecules

L5 ANSWER 5 OF 74 USPATFULL on STN
 TI Single molecule arrays for genetic and chemical analysis

L5 ANSWER 6 OF 74 USPATFULL on STN
 TI Methods of Analysis of Polymorphisms and Uses Thereof

L5 ANSWER 7 OF 74 USPATFULL on STN
 TI Selective cloning of homoduplex nucleic acids

L5 ANSWER 8 OF 74 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 1
 TI The structure of a fibril-forming sequence, NNQQNY, in the context of a globular fold

L5 ANSWER 9 OF 74 USPATFULL on STN DUPLICATE 2
 TI Modified dna cleavage enzymes and methods for use (as amended by isa)

L5 ANSWER 10 OF 74 USPATFULL on STN
 TI Methods for assembly of high fidelity synthetic polynucleotides

L5 ANSWER 11 OF 74 USPATFULL on STN
 TI Methods for assembly of high fidelity synthetic polynucleotides

L5 ANSWER 12 OF 74 USPATFULL on STN
 TI Single molecule arrays for genetic and chemical analysis

L5 ANSWER 13 OF 74 USPATFULL on STN
 TI Methods and compositions for assessment of pulmonary function and disorders

L5 ANSWER 14 OF 74 USPATFULL on STN
 TI Array oligomer synthesis and use

L5 ANSWER 15 OF 74 USPATFULL on STN
 TI Making nucleic acid sequences in parallel and use

L5 ANSWER 16 OF 74 USPATFULL on STN
 TI Mobility-Modified Nucleobase Polymers and Methods of Using Same

L5 ANSWER 17 OF 74 WPIDS COPYRIGHT 2009 THOMSON REUTERS on STN
 TI Repairing a damaged polynucleotide to enhance fidelity or yield of its

copied or amplified product by incubating the polynucleotide in a reaction mixture comprising and enhancing fidelity or yield of the copied or amplified product

- L5 ANSWER 18 OF 74 LIFESCI COPYRIGHT 2009 CSA on STN DUPLICATE 3
TI The Mechanism of the Amyloidogenic Conversion of T7 Endonuclease I
- L5 ANSWER 19 OF 74 USPATFULL on STN DUPLICATE 4
TI Repair of nucleic acids for improved amplification
- L5 ANSWER 20 OF 74 USPATFULL on STN
TI Methods and compositions for assessment of pulmonary function and disorders
- L5 ANSWER 21 OF 74 USPATFULL on STN
TI Methods of analysis of polymorphisms and uses thereof
- L5 ANSWER 22 OF 74 USPATFULL on STN
TI Methods and compositions for assessment of pulmonary function and disorders
- L5 ANSWER 23 OF 74 USPATFULL on STN
TI Methods for assembly of high fidelity synthetic polynucleotides
- L5 ANSWER 24 OF 74 USPATFULL on STN
TI Populations of reporter sequences and methods of their use
- L5 ANSWER 25 OF 74 USPATFULL on STN
TI Error reduction in automated gene synthesis
- L5 ANSWER 26 OF 74 USPATFULL on STN
TI Polynucleotide synthesis
- L5 ANSWER 27 OF 74 USPATFULL on STN
TI Preparation of defined highly labeled probes
- L5 ANSWER 28 OF 74 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 5
TI Alteration of DNA cleaving enzyme activity by changing reciprocal stereo-geometric positions of two catalytic centers, and use of the enzyme for the identification of an SNP
- L5 ANSWER 29 OF 74 USPATFULL on STN
TI Selective cloning of homoduplex nucleic acids
- L5 ANSWER 30 OF 74 USPATFULL on STN
TI Methods and compositions for whole genome amplification and genotyping
- L5 ANSWER 31 OF 74 USPATFULL on STN
TI Charge and mass tags for detection and analysis
- L5 ANSWER 32 OF 74 USPATFULL on STN
TI Methods and compositions for whole genome amplification and genotyping
- L5 ANSWER 33 OF 74 USPATFULL on STN
TI Methods and compositions for whole genome amplification and genotyping
- L5 ANSWER 34 OF 74 USPATFULL on STN
TI Mobility-modified nucleobase polymers and methods of using same
- L5 ANSWER 35 OF 74 USPATFULL on STN
TI Methods and compositions for whole genome amplification and genotyping

L5 ANSWER 36 OF 74 USPATFULL on STN
TI Detection of target molecules through interaction with probes

L5 ANSWER 37 OF 74 USPATFULL on STN
TI Synthetic peptides and uses therefore

L5 ANSWER 38 OF 74 USPATFULL on STN
TI Selective cloning of homoduplex nucleic acids

L5 ANSWER 39 OF 74 USPATFULL on STN
TI Endonuclease VII cloning method

L5 ANSWER 40 OF 74 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
STN DUPLICATE 6
TI Changing the enzymatic activity of T7 endonuclease by mutations at the
beta-bridge site: Alteration of substrate specificity profile and
metal ion requirements by mutation distant from the catalytic domain.

L5 ANSWER 41 OF 74 USPATFULL on STN
TI Maxam gilbert g/a sequence analysis by DHPLC

L5 ANSWER 42 OF 74 USPATFULL on STN
TI Mobility-modified nucleobase polymers and methods of using same

L5 ANSWER 43 OF 74 USPATFULL on STN
TI Method for DNA footprinting

L5 ANSWER 44 OF 74 USPATFULL on STN
TI Fixed address analysis of sequence tags

L5 ANSWER 45 OF 74 USPATFULL on STN
TI Method for detecting and identifying mutations

L5 ANSWER 46 OF 74 USPATFULL on STN
TI Fixed address analysis of sequence tags

L5 ANSWER 47 OF 74 LIFESCI COPYRIGHT 2009 CSA on STN DUPLICATE 7
TI Evaluation of PCR-generated chimeras, mutations, and heteroduplexes with
16S rRNA gene-based cloning

L5 ANSWER 48 OF 74 USPATFULL on STN
TI Detection of mutation by resolvase cleavage

L5 ANSWER 49 OF 74 USPATFULL on STN
TI Detection of mutation by resolvase cleavage

L5 ANSWER 50 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa)
(PublishedApplication)

L5 ANSWER 51 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa)
(PublishedApplication)

L5 ANSWER 52 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa)
(PublishedApplication)

L5 ANSWER 53 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa)
(PublishedApplication)

[illegible]

(PublishedApplication)

L5 ANSWER 70 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa)
(PublishedApplication)

L5 ANSWER 71 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa)
(PublishedApplication)

L5 ANSWER 72 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa)
(PublishedApplication)

L5 ANSWER 73 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa)
(PublishedApplication)

L5 ANSWER 74 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa)
(PublishedApplication)

-> d ibib abs 15 8-10 17 28 32 39-40

L5 ANSWER 8 OF 74 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 1
ACCESSION NUMBER: 2008:1098323 CAPLUS
DOCUMENT NUMBER: 149:507387
TITLE: The structure of a fibril-forming sequence, NNQQNY, in
the context of a globular fold
AUTHOR(S): Gao, Zhefeng; Eisenberg, David
CORPORATE SOURCE: Howard Hughes Medical Institute, UCLA-DOE Institute
for Genomics and Proteomics, Molecular Biology
Institute, UCLA, Los Angeles, CA, 90095-1570, USA
SOURCE: Protein Science (2008), 17(9), 1617-1623
CODEN: PRCL; ISSN: 0961-8368
PUBLISHER: Cold Spring Harbor Laboratory Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Numerous human disorders are associated with the formation of protein
fibrils. The fibril-forming capacity of a protein has been found in
recent studies to be determined by a short segment of residues that forms a
dual β -sheet, called a steric zipper, in the spine of the
fibril. The question arises as to whether a fibril-forming segment, when
inserted within the sequence of a globular protein, will invariably cause
the protein to form fibrils. Here we investigate this question by
inserting the known fibril-forming segment NNQQNY into the
globular enzyme, T7 endonuclease I. From
earlier studies, we know that in its fibril form, NNQQNY is in an extended
conformation. We first found that the inserted NNQQNY
stimulates fibril formation of T7 endonuclease
I in solution. Thus NNQQNY within T7 endonuclease I can exist in an
extended conformation, capable of forming the steric zipper in the core of
a fibril. We also found that T7 endonuclease I folds into a decamer that
does not form fibrils. We determined the structure of the decamer by X-ray
crystallog., finding an unusual oligomer without point group symmetry, and
finding that the NNQQNY segments within the decamer adopt two twisted
conformations, neither is apparently able to fibrillize. We conclude that
twisting of fibril forming sequences from the fully extended conformation,
imposed by the context of their placement in proteins, can interfere with
fibril formation.

REFERENCE COUNT: 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS

RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 9 OF 74 USPATFULL on STN DUPLICATE 2
 ACCESSION NUMBER: 2007:48556 USPATFULL
 TITLE: Modified dna cleavage enzymes and methods for use (as amended by isa)
 INVENTOR(S): Guan, Chudi, Wenham, MA, UNITED STATES
 Kumar, Sanjay, Ipswitch, MA, UNITED STATES
 Kucera, Rebecca, Hamilton, MA, UNITED STATES
 PATENT ASSIGNEE(S): New England Biolabs, Inc., Ipswich, MA, UNITED STATES, 01938 (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 20070042379	A1	20070222
APPLICATION INFO.:	US 2004-585964	A1	20041122 (10)
	WO 2004-US39288		20041122
			20060713 PCT 371 date

DOCUMENT TYPE: Utility
 FILE SEGMENT: APPLICATION
 LEGAL REPRESENTATIVE: HARRIET M. STRIMPEL, NEW ENGLAND BIOLABS, INC., 240 COUNTY ROAD, IPSWICH, MA, 01938-2723, US
 NUMBER OF CLAIMS: 31
 EXEMPLARY CLAIM: 1
 NUMBER OF DRAWINGS: 22 Drawing Page(s)
 LINE COUNT: 1360
 AB Compositions and methods are provided that relate to a modified DNA cleaving enzyme having at least 35% amino acid sequence identity with T7 Endo I. The modified enzyme includes two catalytic centers separated by a .beta .-bridge where the β -bridge contains at least one mutation having an effect of altering enzyme cleavage activity compared to the unmodified enzyme. Activities associated with the modified DNA cleaving enzyme that can be modulated in different reaction conditions include at least one of: (a) non-sequence specific nicking activity; (b) cleaving the second strand of a duplex DNA at a preexisting nick site to produce a linear duplex with a single strand overhang; (c) non-sequence specific DNA cleavage; (d) cleaving DNA flanking a mismatch; and (e) cleavage at a cruciform structure in a DNA duplex.

L5 ANSWER 10 OF 74 USPATFULL on STN
 ACCESSION NUMBER: 2007:308772 USPATFULL
 TITLE: Methods for assembly of high fidelity synthetic polynucleotides
 INVENTOR(S): Church, George, Brookline, MA, UNITED STATES
 Afeyan, Noubar, Lexington, MA, UNITED STATES
 Jacobson, Joseph, Newton, MA, UNITED STATES
 Baynes, Brian M., Somerville, MA, UNITED STATES
 Nesmith, Kenneth Gabriel, Cambridge, MA, UNITED STATES
 Chapman, Brad Alan, Somerville, MA, UNITED STATES
 Strack-Logue, Bettina, Somerville, MA, UNITED STATES

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 20070269870	A1	20071122
APPLICATION INFO.:	US 2005-254250	A1	20051018 (11)
RELATED APPLN. INFO.:	Continuation-in-part of Ser. No. US 2005-68321, filed on 28 Feb 2005, PENDING Continuation-in-part of Ser. No. US 2005-67812, filed on 28 Feb 2005, PENDING		

	NUMBER	DATE
PRIORITY INFORMATION:	US 2004-619650P	20041018 (60)
	US 2005-657014P	20050228 (60)
	US 2005-698560P	20050712 (60)
	US 2005-643813P	20050113 (60)
	US 2005-727205P	20051014 (60)
DOCUMENT TYPE:	Utility	
FILE SEGMENT:	APPLICATION	
LEGAL REPRESENTATIVE:	ROPES & GRAY LLP, PATENT DOCKETING 39/41, ONE INTERNATIONAL PLACE, BOSTON, MA, 02110-2624, US	
NUMBER OF CLAIMS:	21	
EXEMPLARY CLAIM:	1-291	
NUMBER OF DRAWINGS:	36 Drawing Page(s)	
LINE COUNT:	5051	

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Disclosed are methods of manufacturing synthetic DNAs, that is, DNAs made at least in significant part by chemical synthesis of nucleic acid polymers. Also provided are methods for assembling plural DNAs in the same pool by multiplexed assembly of synthetic oligonucleotides. In exemplary embodiments, the methods involve pre-amplification of one or more oligonucleotides using "universal" primers, reduction of the error rate in oligonucleotide and/or nucleic acid products, and sequence optimization and oligonucleotides design. Also provided are low-purity arrays of nucleic acids and methods for assembling nucleic acids using oligonucleotides obtained from low-purity arrays.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 17 OF 74 WPIDS COPYRIGHT 2009 THOMSON REUTERS on STN
 ACCESSION NUMBER: 2007-805625 [75] WPIDS
 DOC. NO. CPI: C2007-279817 [75]
 TITLE: Repairing a damaged polynucleotide to enhance fidelity or yield of its copied or amplified product by incubating the polynucleotide in a reaction mixture comprising and enhancing fidelity or yield of the copied or amplified product
 DERWENT CLASS: B04; D16
 INVENTOR: CHEN L; EVANS T C; GUAN C; KUCERA R; SLATKO B; VAISVILA R; EVANS T
 PATENT ASSIGNEE: (NEWE-C) NEW ENGLAND BIOLABS INC
 COUNTRY COUNT: 119

PATENT INFO ABBR.:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN IPC
WO 2007120627	A2	20071025	(200775)*	EN	137[20]	
WO 2007120627	A3	20071227	(200803)	EN		
EP 2010678	A2	20090107	(200906)	EN		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2007120627	A2	WO 2007-US8792	20070411
EP 2010678	A2	EP 2007-755155	20070411
EP 2010678	A2	PCT Application	WO 2007-US8792 20070411

FILING DETAILS:

PATENT NO	KIND	PATENT NO
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EP 2010678 A2 Based on WO 2007120627 A

PRIORITY APPLN. INFO: US 2006-791056P 20060411

AN 2007-805625 [75] WPIDS

AB WO 2007120627 A2 UPAB: 20090130

NOVELTY - Repairing a damaged polynucleotide so as to enhance at least one of fidelity and yield of a copied or amplified product of the polynucleotide comprises incubating the polynucleotide in a reaction mixture comprising apurinic/apyrimidinic (AP) endonuclease; a DNA ligase; and NAD or ATP as a cofactor; and enhancing fidelity or yield of the copied or amplified product.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are:

- (1) a kit;
- (2) a polynucleotide repair mixture;
- (3) a method for cloning or sequencing a polynucleotide fragment;
- (4) a method for enhancing the yield of a copied or amplified polynucleotide;
- (5) a method for sequencing a polynucleotide; and
- (6) a method for copying or amplifying a fragmented DNA.

USE - The method is useful in repairing a damaged polynucleotide so as to enhance fidelity or yield of a copied or amplified product of the polynucleotide (claimed).

L5 ANSWER 28 OF 74 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 5

ACCESSION NUMBER: 2005:490414 CAPLUS

DOCUMENT NUMBER: 143:40003

TITLE: Alteration of DNA cleaving enzyme activity by changing reciprocal stereo-geometric positions of two catalytic centers, and use of the enzyme for the identification of an SNP

INVENTOR(S): Guan, Chudi; Kumar, Sanjay; Kucera, Rebecca

PATENT ASSIGNEE(S): New England Biolabs, Inc., USA

SOURCE: PCT Int. Appl., 80 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2005052124	A2	20050609	WO 2004-US39288	20041122
WO 2005052124	A3	20051027		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
EP 1702063	A2	20060920	EP 2004-811921	20041122
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, FI, RO, CY, TR, BG, CZ, EE, HU, PL, SK, IS				
CN 1906292	A	20070131	CN 2004-80040697	20041122
IN 2006DN03516	A	20070831	IN 2006-DN3516	20060619
US 20070042379	A1	20070222	US 2006-585964	20060713
PRIORITY APPLN. INFO.:			US 2003-524123P	P 20031121

AB Comps. and methods are provided that relate to a modified DNA cleaving enzyme having at least 35% amino acid sequence identity with T7 endonuclease I (T7 Endo I). The modified enzyme includes two catalytic centers separated by a β -bridge where the β -bridge contains at least one mutation having an effect of altering enzyme cleavage activity compared to the unmodified enzyme. Activities associated with the modified DNA cleaving enzyme that can be modulated in different reaction conditions include at least one of: (a) non-sequence specific nicking activity; (b) cleaving the second strand of a duplex DNA at a preexisting nick site to produce a linear duplex with a single strand overhang; (c) non-sequence specific DNA cleavage; (d) cleaving DNA flanking a mismatch; and (e) cleavage at a cruciform structure in a DNA duplex. The modified DNA cleaving enzyme can be used for the identification of the location of an SNP. A feature of the modified T7 Endo I is reduced toxicity in a host cell permitting overexpression of the DNA cleaving enzyme.

L5 ANSWER 32 OF 74 USPATFULL on STN

ACCESSION NUMBER: 2005:68909 USPATFULL
 TITLE: Methods and compositions for whole genome amplification and genotyping
 INVENTOR(S): Gunderson, Kevin, Encinitas, CA, UNITED STATES
 Steemers, Frank, San Diego, CA, UNITED STATES
 PATENT ASSIGNEE(S): Illumina, Inc., San Diego, CA (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 20050059048	A1	20050317
APPLICATION INFO.:	US 2004-872141	A1	20040617 (10)
RELATED APPLN. INFO.:	Continuation-in-part of Ser. No. US 2003-681800, filed on 8 Oct 2003, PENDING Continuation of Ser. No. US 2003-600634, filed on 20 Jun 2003, PENDING		
DOCUMENT TYPE:	Utility		
FILE SEGMENT:	APPLICATION		
LEGAL REPRESENTATIVE:	John T. Murphy, Illumina, Inc., 9885 Towne Centre Drive, San Diego, CA, 92121-1975		
NUMBER OF CLAIMS:	52		
EXEMPLARY CLAIM:	CLM-01-77		
NUMBER OF DRAWINGS:	18 Drawing Page(s)		
LINE COUNT:	5277		

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB This invention provides methods of amplifying genomic DNA to obtain an amplified representative population of genome fragments. Methods are further provided for obtaining amplified genomic DNA representations of a desired complexity. The invention further provides methods for simultaneously detecting large numbers of typable loci for an amplified representative population of genome fragments. Accordingly the methods can be used to genotype individuals on a genome-wide scale.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 39 OF 74 USPATFULL on STN

ACCESSION NUMBER: 2004:2134 USPATFULL
 TITLE: Endonuclease VII cloning method
 INVENTOR(S): Greener, Alan L., San Diego, CA, UNITED STATES
 Hexdall, Lisa Joy, San Diego, CA, UNITED STATES
 Carstens, Carsten-Peter, San Diego, CA, UNITED STATES
 Sorge, Joseph A., Wilson, WY, UNITED STATES
 PATENT ASSIGNEE(S): Stratagene (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 20040002155	A1	20040101
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LEGAL REPRESENTATIVE:	PALMER & DODGE, LLP, KATHLEEN M. WILLIAMS / STR, 111 HUNTINGTON AVENUE, BOSTON, MA, 02199		
NUMBER OF CLAIMS:	38		
EXEMPLARY CLAIM:	1		
NUMBER OF DRAWINGS:	4 Drawing Page(s)		
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CAS INDEXING IS AVAILABLE FOR THIS PATENT.			
AB	The subject invention provides for a strain of host cells that contains a temperature sensitive variant of the gene encoding the endonuclease VII from phage T4. Using this host strain, the invention features a novel cloning method that selects for PCR products that are devoid of PCR-generated mutations.		

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 40 OF 74 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
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ACCESSION NUMBER: 2004:267671 BIOSIS
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TITLE: Changing the enzymatic activity of T7 endonuclease by mutations at the beta-bridge site: Alteration of substrate specificity profile and metal ion requirements by mutation distant from the catalytic domain.

AUTHOR(S): Guan, Chudi [Reprint Author]; Kumar, Sanjay; Kucera, Rebecca; Ewel, Amy

CORPORATE SOURCE: New England Biolabs Inc, 32 Tozer Rd, Beverly, MA, 01915, USA
Guan@neb.com

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AB Phage-encoded resolvase T7 endonuclease I is a structure-specific endonuclease. The enzyme acts on a broad spectrum of substrates with a variety of DNA structures. The enzyme is a dimer with two separated catalytic domains connected by an elongated beta-sheet bridge. The activities of enzymes with mutations in the beta-bridge segment were studied. Mutations that did not affect catalytic domain folding and function but did alter the relative positions of these domains retained catalytic activity but with altered specificity and metal ion dependence. Our results suggest that the enzyme recognizes its substrates by DNA conformation exclusion and offer a simple explanation for the broad substrate specificity of phage resolvase.

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(FILE 'HOME' ENTERED AT 23:44:57 ON 01 FEB 2009)

INDEX 'ADISCT1, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEARA-VTB, CIN, CONFSCI, CROFB, CROPU, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 23:45:17 ON 01 FEB 2009

SEA T7 (3A) (ENDO OR ENDONUCLEAS?) (3A) (1 OR I)

2 FILE AGRICOLA
5 FILE BIOENG
62 FILE BIOSIS
18 FILE BIOTECHABS
18 FILE BIOTECHDS
27 FILE BIOTECHNO
88 FILE CAPLUS
59 FILE DGENE
2 FILE DISSABS
1 FILE DRUGU
50 FILE EMBASE
38 FILE ESBIOBASE
57 FILE GENRANK
34 FILE IFIPAT
40 FILE LIFESCI
56 FILE MEDLINE
12 FILE PASCAL
66 FILE SCISEARCH
21 FILE TOXCENTER
25 FILE USGENE
103 FILE USPATFULL
14 FILE USPAT2
25 FILE WPIDS
25 FILE WPINDEX

L1 QUE T7 (3A) (ENDO OR ENDONUCLEAS?) (3A) (1 OR I)

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FILE 'USPATFULL, CAPLUS, SCISEARCH, BIOSIS, MEDLINE, EMBASE, LIFESCI,
ESBIOBASE, IFIPAT, BIOTECHNO, USGENE, WPIDS' ENTERED AT 23:48:56 ON 01
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L2 614 SEA T7 (3A) (ENDO OR ENDONUCLEAS?) (3A) (1 OR I)
L3 203 SEA L2(S) (MODIF? OR MUTA? OR DELET? OR INSER?)
L4 89 SEA L3 AND BETA?
L5 74 DUP REM L4 (15 DUPLICATES REMOVED)
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FILE HOME

FILE STNINDEX

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